#6

SEQUENCE LISTING

<110> Edwin L. Madison
Edgar O. Ong

<120> NUCLEIC ACID MOLECULES ENCODING TRANSMEMBRANE SERINE PROTEASE 7, THE ENCODED POLYPEPTIDES AND METHODS BASED THEREON

<130> 24745-1613

<140>
<141> Herewith

<150> 60/275,592
<151> 2001-03-13

<160> 22

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 3147
<212> DNA
<213> Homo Sapien

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<221> CDS
<222> (23)...(2589)
<223> Nucleotide sequence encoding MTSP1

<300>
<301> O'Brien, T.J. and Tanimoto, H.
<308> GenBank #AR081724
<309> 2000-08-31
<310> 5,972,616
<311> 1998-02-20
<312> 1999-10-26

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ggg ggc ccg aag gac ttc ggc gcg gga ctc aag tac aac tcc cgg cac      100
Gly Gly Pro Lys Asp Phe Gly Ala Gly Leu Lys Tyr Asn Ser Arg His
                 15                  20                  25

gag aaa gtg aat ggc ttg gag gaa ggc gtg gag ttc ctg cca gtc aac      148
Glu Lys Val Asn Gly Leu Glu Glu Gly Val Glu Phe Leu Pro Val Asn
             30                  35                  40

aac gtc aag aag gtg gaa aag cat ggc ccg ggg cgc tgg gtg gtg ctg      196
Asn Val Lys Lys Val Glu Lys His Gly Pro Gly Arg Trp Val Val Leu
         45                  50                  55

gca gcc gtg ctg atc ggc ctc ctc ttg gtc ttg ctg ggg atc ggc ttc      244
Ala Ala Val Leu Ile Gly Leu Leu Leu Val Leu Leu Gly Ile Gly Phe
     60                  65                  70

ctg gtg tgg cat ttg cag tac cgg gac gtg cgt gtc cag aag gtc ttc      292
Leu Val Trp His Leu Gln Tyr Arg Asp Val Arg Val Gln Lys Val Phe
 75                  80                  85                  90

aat ggc tac atg agg atc aca aat gag aat ttt gtg gat gcc tac gag      340
Asn Gly Tyr Met Arg Ile Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu
                 95                 100                 105
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aac tcc aac tcc act gag ttt gta agc ctg gcc agc aag gtg aag gac      388
Asn Ser Asn Ser Thr Glu Phe Val Ser Leu Ala Ser Lys Val Lys Asp
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gcg ctg aag ctg ctg tac agc gga gtc cca ttc ctg ggc ccc tac cac      436
Ala Leu Lys Leu Leu Tyr Ser Gly Val Pro Phe Leu Gly Pro Tyr His
        125                 130                 135

aag gag tcg gct gtg acg gcc ttc agc gag ggc agc gtc atc gcc tac      484
Lys Glu Ser Ala Val Thr Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr
    140                 145                 150

tac tgg tct gag ttc agc atc ccg cag cac ctg gtg gag gag gcc gag      532
Tyr Trp Ser Glu Phe Ser Ile Pro Gln His Leu Val Glu Glu Ala Glu
155                 160                 165                 170

cgc gtc atg gcc gag gag cgc gta gtc atg ctg ccc ccg cgg gcg cgc      580
Arg Val Met Ala Glu Glu Arg Val Val Met Leu Pro Pro Arg Ala Arg
                175                 180                 185

tcc ctg aag tcc ttt gtg gtc acc tca gtg gtg gct ttc ccc acg gac      628
Ser Leu Lys Ser Phe Val Val Thr Ser Val Val Ala Phe Pro Thr Asp
            190                 195                 200

tcc aaa aca gta cag agg acc cag gac aac agc tgc agc ttt ggc ctg      676
Ser Lys Thr Val Gln Arg Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu
        205                 210                 215

cac gcc cgc ggt gtg gag ctg atg cgc ttc acc acg ccc ggc ttc cct      724
His Ala Arg Gly Val Glu Leu Met Arg Phe Thr Thr Pro Gly Phe Pro
    220                 225                 230

gac agc ccc tac ccc gct cat gcc cgc tgc cag tgg gcc ctg cgg ggg      772
Asp Ser Pro Tyr Pro Ala His Ala Arg Cys Gln Trp Ala Leu Arg Gly
235                 240                 245                 250

gac gcc gac tca gtg ctg agc ctc acc ttc cgc agc ttt gac ctt gcg      820
Asp Ala Asp Ser Val Leu Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala
                255                 260                 265

tcc tgc gac gag cgc ggc agc gac ctg gtg acg gtg tac aac acc ctg      868
Ser Cys Asp Glu Arg Gly Ser Asp Leu Val Thr Val Tyr Asn Thr Leu
            270                 275                 280

agc ccc atg gag ccc cac gcc ctg gtg cag ttg tgt ggc acc tac cct      916
Ser Pro Met Glu Pro His Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro
        285                 290                 295

ccc tcc tac aac ctg acc ttc cac tcc tcc cag aac gtc ctg ctc atc      964
Pro Ser Tyr Asn Leu Thr Phe His Ser Ser Gln Asn Val Leu Leu Ile
    300                 305                 310

aca ctg ata acc aac act gag cgg cgg cat ccc ggc ttt gag gcc acc     1012
Thr Leu Ile Thr Asn Thr Glu Arg Arg His Pro Gly Phe Glu Ala Thr
315                 320                 325                 330

ttc ttc cag ctg cct agg atg agc agc tgt gga ggc cgc tta cgt aaa     1060
Phe Phe Gln Leu Pro Arg Met Ser Ser Cys Gly Gly Arg Leu Arg Lys
                335                 340                 345

gcc cag ggg aca ttc aac agc ccc tac tac cca ggc cac tac cca ccc     1108
Ala Gln Gly Thr Phe Asn Ser Pro Tyr Tyr Pro Gly His Tyr Pro Pro
            350                 355                 360

aac att gac tgc aca tgg aac att gag gtg ccc aac aac cag cat gtg     1156
Asn Ile Asp Cys Thr Trp Asn Ile Glu Val Pro Asn Asn Gln His Val
        365                 370                 375
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aag gtg agc ttc aaa ttc ttc tac ctg ctg gag ccc ggc gtg cct gcg      1204
Lys Val Ser Phe Lys Phe Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala
    380                 385                 390

ggc acc tgc ccc aag gac tac gtg gag atc aat ggg gag aaa tac tgc      1252
Gly Thr Cys Pro Lys Asp Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys
395                 400                 405                 410

gga gag agg tcc cag ttc gtc gtc acc agc aac agc aac aag atc aca      1300
Gly Glu Arg Ser Gln Phe Val Val Thr Ser Asn Ser Asn Lys Ile Thr
                415                 420                 425

gtt cgc ttc cac tca gat cag tcc tac acc gac acc ggc ttc tta gct      1348
Val Arg Phe His Ser Asp Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala
            430                 435                 440

gaa tac ctc tcc tac gac tcc agt gac cca tgc ccg ggg cag ttc acg      1396
Glu Tyr Leu Ser Tyr Asp Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr
        445                 450                 455

tgc cgc acg ggg cgg tgt atc cgg aag gag ctg cgc tgt gat ggc tgg      1444
Cys Arg Thr Gly Arg Cys Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp
    460                 465                 470

gcc gac tgc acc gac cac agc gat gag ctc aac tgc agt tgc gac gcc      1492
Ala Asp Cys Thr Asp His Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala
475                 480                 485                 490

ggc cac cag ttc acg tgc aag aac aag ttc tgc aag ccc ctc ttc tgg      1540
Gly His Gln Phe Thr Cys Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp
                495                 500                 505

gtc tgc gac agt gtg aac gac tgc gga gac aac agc gac gag cag ggg      1588
Val Cys Asp Ser Val Asn Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly
            510                 515                 520

tgc agt tgt ccg gcc cag acc ttc agg tgt tcc aat ggg aag tgc ctc      1636
Cys Ser Cys Pro Ala Gln Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu
        525                 530                 535

tcg aaa agc cag cag tgc aat ggg aag gac gac tgt ggg gac ggg tcc      1684
Ser Lys Ser Gln Gln Cys Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser
    540                 545                 550

gac gag gcc tcc tgc ccc aag gtg aac gtc gtc act tgt acc aaa cac      1732
Asp Glu Ala Ser Cys Pro Lys Val Asn Val Val Thr Cys Thr Lys His
555                 560                 565                 570

acc tac cgc tgc ctc aat ggg ctc tgc ttg agc aag ggc aac cct gag      1780
Thr Tyr Arg Cys Leu Asn Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu
                575                 580                 585

tgt gac ggg aag gag gac tgt agc gac ggc tca gat gag aag gac tgc      1828
Cys Asp Gly Lys Glu Asp Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys
            590                 595                 600

gac tgt ggg ctg cgg tca ttc acg aga cag gct cgt gtt gtt ggg ggc      1876
Asp Cys Gly Leu Arg Ser Phe Thr Arg Gln Ala Arg Val Val Gly Gly
        605                 610                 615

acg gat gcg gat gag ggc gag tgg ccc tgg cag gta agc ctg cat gct      1924
Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val Ser Leu His Ala
    620                 625                 630

ctg ggc cag ggc cac atc tgc ggt gct tcc ctc atc tct ccc aac tgg      1972
Leu Gly Gln Gly His Ile Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp
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635                 640                 645                 650

ctg gtc tct gcc gca cac tgc tac atc gat gac aga gga ttc agg tac     2020
Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr
                655                 660                 665

tca gac ccc acg cag tgg acg gcc ttc ctg ggc ttg cac gac cag agc     2068
Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu His Asp Gln Ser
            670                 675                 680

cag cgc agc gcc cct ggg gtg cag gag cgc agg ctc aag cgc atc atc     2116
Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu Lys Arg Ile Ile
        685                 690                 695

tcc cac ccc ttc ttc aat gac ttc acc ttc gac tat gac atc gcg ctg     2164
Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp Tyr Asp Ile Ala Leu
    700                 705                 710

ctg gag ctg gag aaa ccg gca gag tac agc tcc atg gtg cgg ccc atc     2212
Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met Val Arg Pro Ile
715                 720                 725                 730

tgc ctg ccg gac gcc tcc cat gtc ttc cct gcc ggc aag gcc atc tgg     2260
Cys Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly Lys Ala Ile Trp
                735                 740                 745

gtc acg ggc tgg gga cac acc cag tat gga ggc act ggc gcg ctg atc     2308
Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile
            750                 755                 760

ctg caa aag ggt gag atc cgc gtc atc aac cag acc acc tgc gag aac     2356
Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr Thr Cys Glu Asn
        765                 770                 775

ctc ctg ccg cag cag atc acg ccg cgc atg atg tgc gtg ggc ttc ctc     2404
Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys Val Gly Phe Leu
    780                 785                 790

agc ggc ggc gtg gac tcc tgc cag ggt gat tcc ggg gga ccc ctg tcc     2452
Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser
795                 800                 805                 810

agc gtg gag gcg gat ggg cgg atc ttc cag gcc ggt gtg gtg agc tgg     2500
Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly Val Val Ser Trp
                815                 820                 825

gga gac ggc tgc gct cag agg aac aag cca ggc gtg tac aca agg ctc     2548
Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu
            830                 835                 840

cct ctg ttt cgg gac tgg atc aaa gag aac act ggg gta ta ggggccgggg   2599
Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly Val
        845                 850                 855

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aaaaaaaa                                                           3147

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<212> PRT
<213> Homo Sapien

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            20                  25                  30
Glu Glu Gly Val Glu Phe Leu Pro Val Asn Asn Val Lys Lys Val Glu
        35                  40                  45
Lys His Gly Pro Gly Arg Trp Val Val Leu Ala Ala Val Leu Ile Gly
    50                  55                  60
Leu Leu Leu Val Leu Leu Gly Ile Gly Phe Leu Val Trp His Leu Gln
65                  70                  75                  80
Tyr Arg Asp Val Arg Val Gln Lys Val Phe Asn Gly Tyr Met Arg Ile
                85                  90                  95
Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu Asn Ser Asn Ser Thr Glu
            100                 105                 110
Phe Val Ser Leu Ala Ser Lys Val Lys Asp Ala Leu Lys Leu Leu Tyr
        115                 120                 125
Ser Gly Val Pro Phe Leu Gly Pro Tyr His Lys Glu Ser Ala Val Thr
    130                 135                 140
Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp Ser Glu Phe Ser
145                 150                 155                 160
Ile Pro Gln His Leu Val Glu Glu Ala Glu Arg Val Met Ala Glu Glu
                165                 170                 175
Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu Lys Ser Phe Val
            180                 185                 190
Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys Thr Val Gln Arg
        195                 200                 205
Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu
    210                 215                 220
Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser Pro Tyr Pro Ala
225                 230                 235                 240
His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala Asp Ser Val Leu
                245                 250                 255
Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys Asp Glu Arg Gly
            260                 265                 270
Ser Asp Leu Val Thr Val Tyr Asn Thr Leu Ser Pro Met Glu Pro His
        275                 280                 285
Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro Pro Ser Tyr Asn Leu Thr
    290                 295                 300
Phe His Ser Ser Gln Asn Val Leu Leu Ile Thr Leu Ile Thr Asn Thr
305                 310                 315                 320
Glu Arg Arg His Pro Gly Phe Glu Ala Thr Phe Phe Gln Leu Pro Arg
                325                 330                 335
Met Ser Ser Cys Gly Gly Arg Leu Arg Lys Ala Gln Gly Thr Phe Asn
            340                 345                 350
Ser Pro Tyr Tyr Pro Gly His Tyr Pro Pro Asn Ile Asp Cys Thr Trp
        355                 360                 365
Asn Ile Glu Val Pro Asn Asn Gln His Val Lys Val Ser Phe Lys Phe
    370                 375                 380
Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala Gly Thr Cys Pro Lys Asp
385                 390                 395                 400
Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys Gly Glu Arg Ser Gln Phe
                405                 410                 415
Val Val Thr Ser Asn Ser Asn Lys Ile Thr Val Arg Phe His Ser Asp
            420                 425                 430
Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala Glu Tyr Leu Ser Tyr Asp
        435                 440                 445
Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr Cys Arg Thr Gly Arg Cys
    450                 455                 460
Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp Ala Asp Cys Thr Asp His
465                 470                 475                 480
Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala Gly His Gln Phe Thr Cys
                485                 490                 495
Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp Val Cys Asp Ser Val Asn
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Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly Cys Ser Cys Pro Ala Gln
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Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu Ser Lys Ser Gln Gln Cys
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Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser Asp Glu Ala Ser Cys Pro
545                 550                 555                 560
Lys Val Asn Val Val Thr Cys Thr Lys His Thr Tyr Arg Cys Leu Asn
                565                 570                 575
Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu Cys Asp Gly Lys Glu Asp
            580                 585                 590
Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys Asp Cys Gly Leu Arg Ser
        595                 600                 605
Phe Thr Arg Gln Ala Arg Val Val Gly Gly Thr Asp Ala Asp Glu Gly
    610                 615                 620
Glu Trp Pro Trp Gln Val Ser Leu His Ala Leu Gly Gln Gly His Ile
625                 630                 635                 640
Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His
                645                 650                 655
Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp
            660                 665                 670
Thr Ala Phe Leu Gly Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly
        675                 680                 685
Val Gln Glu Arg Arg Leu Lys Arg Ile Ile Ser His Pro Phe Phe Asn
    690                 695                 700
Asp Phe Thr Phe Asp Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro
705                 710                 715                 720
Ala Glu Tyr Ser Ser Met Val Arg Pro Ile Cys Leu Pro Asp Ala Ser
                725                 730                 735
His Val Phe Pro Ala Gly Lys Ala Ile Trp Val Thr Gly Trp Gly His
            740                 745                 750
Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile
        755                 760                 765
Arg Val Ile Asn Gln Thr Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile
    770                 775                 780
Thr Pro Arg Met Met Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser
785                 790                 795                 800
Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly
                805                 810                 815
Arg Ile Phe Gln Ala Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln
            820                 825                 830
Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp
        835                 840                 845
Ile Lys Glu Asn Thr Gly Val
    850                 855
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<210> 3
<211> 3147
<212> DNA
<213> Homo Sapien

<220>
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<222> (1865)...(2590)
<223> Nucleic acid sequence of protease domain of MTSP1

<400> 3

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ggaaggcgtg gagttcctgc cagtcaacaa cgtcaagaag gtggaaaagc atggcccggg     180
gcgctgggtg gtgctggcag ccgtgctgat cggcctcctc ttggtcttgc tggggatcgg     240
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tcgt gtt gtt ggg ggc acg gat gcg gat gag ggc gag tgg ccc tgg cag      1909
     Val Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln
      1               5                  10                  15

gta agc ctg cat gct ctg ggc cag ggc cac atc tgc ggt gct tcc ctc      1957
Val Ser Leu His Ala Leu Gly Gln Gly His Ile Cys Gly Ala Ser Leu
                 20                  25                  30

atc tct ccc aac tgg ctg gtc tct gcc gca cac tgc tac atc gat gac      2005
Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp
             35                  40                  45

aga gga ttc agg tac tca gac ccc acg cag tgg acg gcc ttc ctg ggc      2053
Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly
         50                  55                  60

ttg cac gac cag agc cag cgc agc gcc cct ggg gtg cag gag cgc agg      2101
Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg
     65                  70                  75

ctc aag cgc atc atc tcc cac ccc ttc ttc aat gac ttc acc ttc gac      2149
Leu Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp
 80                  85                  90                  95

tat gac atc gcg ctg ctg gag ctg gag aaa ccg gca gag tac agc tcc      2197
Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser
                100                 105                 110

atg gtg cgg ccc atc tgc ctg ccg gac gcc tcc cat gtc ttc cct gcc      2245
Met Val Arg Pro Ile Cys Leu Pro Asp Ala Ser His Val Phe Pro Ala
            115                 120                 125

ggc aag gcc atc tgg gtc acg ggc tgg gga cac acc cag tat gga ggc      2293
Gly Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly
        130                 135                 140

act ggc gcg ctg atc ctg caa aag ggt gag atc cgc gtc atc aac cag      2341
Thr Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln
    145                 150                 155

acc acc tgc gag aac ctc ctg ccg cag cag atc acg ccg cgc atg atg      2389
Thr Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met
160                 165                 170                 175

tgc gtg ggc ttc ctc agc ggc ggc gtg gac tcc tgc cag ggt gat tcc      2437
Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser
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                180                 185                 190

ggg gga ccc ctg tcc agc gtg gag gcg gat ggg cgg atc ttc cag gcc     2485
Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala
            195                 200                 205

ggt gtg gtg agc tgg gga gac ggc tgc gct cag agg aac aag cca ggc     2533
Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly
        210                 215                 220

gtg tac aca agg ctc cct ctg ttt cgg gac tgg atc aaa gag aac act     2581
Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr
    225                 230                 235

ggg gta tag gggccggggc cacccaaatg tgtacacctg cggggccacc             2630
Gly Val  *
240

catcgtccac cccagtgtgc acgcctgcag gctggagact ggaccgctga ctgcaccagc   2690
gccccccagaa catacactgt gaactcaatc tccagggctc caaatctgcc tagaaaacct   2750
ctcgcttcct cagcctccaa agtggagctg ggaggtagaa ggggaggaca ctggtggttc   2810

tactgaccca actgggggca aaggtttgaa gacacagcct cccccgccag ccccaagctg   2870
ggccgaggcg cgtttgtgta tatctgcctc ccctgtctgt aaggagcagc gggaacggag   2930
cttcggagcc tcctcagtga aggtggtggg gctgccggat ctgggctgtg gggcccttgg   2990
gccacgctct tgaggaagcc caggctcgga ggaccctgga aaacagacgg gtctgagact   3050
gaaattgttt taccagctcc cagggtggac ttcagtgtgt gtatttgtgt aaatgggtaa   3110
aacaatttat ttctttttaa aaaaaaaaaa aaaaaaa                            3147

<210> 4
<211> 241
<212> PRT
<213> Homo Sapien

<400> 4
Val Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val
 1               5                  10                  15
Ser Leu His Ala Leu Gly Gln Gly His Ile Cys Gly Ala Ser Leu Ile
            20                  25                  30
Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg
        35                  40                  45
Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu
    50                  55                  60
His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu
65                  70                  75                  80
Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp Tyr
                85                  90                  95
Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met
            100                 105                 110
Val Arg Pro Ile Cys Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly
        115                 120                 125
Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr
    130                 135                 140
Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr
145                 150                 155                 160
Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys
                165                 170                 175
Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
            180                 185                 190
Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly
        195                 200                 205
Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val
    210                 215                 220
Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly
225                 230                 235                 240
Val
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<210> 5
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 5
aatggccatg gcaggccagc ctcc 24

<210> 6
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 6
gtcccaaact tactatacct acaatgtacc ag 32

<210> 7
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 7
gtccccaact tactatacct acaatgtacc ag 32

<210> 8
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 8
aatggccatg gcaggccagc ctcc 24

<210> 9
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 9
tgccattacc agcatcctct tctactcaaa g 31

<210> 10
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 10
ccatgtgtat aactcacgga caatccacac tac 33

<210> 11

<211> 10
<212> PRT
<213> Homo sapien

<400> 11
Met Pro Leu Pro Ala Ser Ser Ser Thr Gln
 1   5   10

<210> 12
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 12
tctctcgaga aaagaattgt ccaaggaagg gaaacagcta tg   42

<210> 13
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 13
atagcggccg cacactacat accagtcttt gaggcaatc   39

<210> 14
<211> 11
<212> PRT
<213> Homo sapien

<400> 14
Lys Arg Ile Val Gln Gly Arg Glu Thr Ala Met
 1   5   10

<210> 15
<211> 2100
<212> DNA
<213> Homo sapien

<220>
<221> CDS
<222> (45)...(1361)
<223> MTSP7: full length cDNA

<220>
<221> CDS
<222> (45)...(1361)
<223> MTSP7: full length cDNA

<400> 15
agatcagatg gcgactgaat agaagctgcc ccagtcctgg gttc atg atg tac aca   56
                                                Met Met Tyr Thr
                                                 1

cct gtt gaa ttt tca gaa gct gaa ttc tca cga gct gaa tat caa aga   104
Pro Val Glu Phe Ser Glu Ala Glu Phe Ser Arg Ala Glu Tyr Gln Arg
 5   10   15   20

aag cag caa ttt tgg gac tca gta cgg cta gct ctt ttc aca tta gca   152
Lys Gln Gln Phe Trp Asp Ser Val Arg Leu Ala Leu Phe Thr Leu Ala
                25   30   35

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att gta gca atc ata gga att gca att ggt att gtt act cat ttt gtt      200
Ile Val Ala Ile Ile Gly Ile Ala Ile Gly Ile Val Thr His Phe Val
            40                  45                  50

gtt gag gat gat aag tct ttc tat tac ctt gcc tct ttt aaa gtc aca      248
Val Glu Asp Asp Lys Ser Phe Tyr Tyr Leu Ala Ser Phe Lys Val Thr
        55                  60                  65

aat atc aaa tat aaa gaa aat tat ggc ata aga tct tca aga gag ttt      296
Asn Ile Lys Tyr Lys Glu Asn Tyr Gly Ile Arg Ser Ser Arg Glu Phe
    70                  75                  80

ata gaa agg agt cat cag att gaa aga atg atg tct agg ata ttt cga      344
Ile Glu Arg Ser His Gln Ile Glu Arg Met Met Ser Arg Ile Phe Arg
 85                  90                  95                  100

cat tct tct gta ggc ggt cga ttt atc aaa tct cat gtt atc aaa tta      392
His Ser Ser Val Gly Gly Arg Phe Ile Lys Ser His Val Ile Lys Leu
                105                 110                 115

agt cca gat gaa caa ggt gtg gat att ctt ata gtg ctc ata ttt cga      440
Ser Pro Asp Glu Gln Gly Val Asp Ile Leu Ile Val Leu Ile Phe Arg
            120                 125                 130

tac cca tct act gat agt gct gaa caa atc aag aaa aaa att gaa aag      488
Tyr Pro Ser Thr Asp Ser Ala Glu Gln Ile Lys Lys Lys Ile Glu Lys
        135                 140                 145

gct tta tat caa agt ttg aag acc aaa caa ttg tct ttg acc ata aac      536
Ala Leu Tyr Gln Ser Leu Lys Thr Lys Gln Leu Ser Leu Thr Ile Asn
    150                 155                 160

aaa cca tca ttt aga ctc aca cct att gac agc aaa aag atg agg aat      584
Lys Pro Ser Phe Arg Leu Thr Pro Ile Asp Ser Lys Lys Met Arg Asn
165                 170                 175                 180

ctt ctc aac agt cgc tgt gga ata agg atg aca tct tca aac atg cca      632
Leu Leu Asn Ser Arg Cys Gly Ile Arg Met Thr Ser Ser Asn Met Pro
                185                 190                 195

tta cca gca tcc tct tct act caa aga att gtc caa gga agg gaa aca      680
Leu Pro Ala Ser Ser Ser Thr Gln Arg Ile Val Gln Gly Arg Glu Thr
            200                 205                 210

gct atg gaa ggg gaa tgg cca tgg cag gcc agc ctc cag ctc ata ggg      728
Ala Met Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu Gln Leu Ile Gly
        215                 220                 225

tca ggc cat cag tgt gga gcc agc ctc atc agt aac aca tgg ctg ctc      776
Ser Gly His Gln Cys Gly Ala Ser Leu Ile Ser Asn Thr Trp Leu Leu
    230                 235                 240

aca gca gct cac tgc ttt tgg aaa aat aaa gac cca act caa tgg att      824
Thr Ala Ala His Cys Phe Trp Lys Asn Lys Asp Pro Thr Gln Trp Ile
245                 250                 255                 260

gct act ttt ggt gca act ata aca cca ccc gca gtg aaa cga aat gtg      872
Ala Thr Phe Gly Ala Thr Ile Thr Pro Pro Ala Val Lys Arg Asn Val
                265                 270                 275

agg aaa att att ctt cat gag aat tac cat aga gaa aca aat gaa aat      920
Arg Lys Ile Ile Leu His Glu Asn Tyr His Arg Glu Thr Asn Glu Asn
            280                 285                 290

gac att gct ttg gtt cag ctc tct act gga gtt gag ttt tca aat ata      968
Asp Ile Ala Leu Val Gln Leu Ser Thr Gly Val Glu Phe Ser Asn Ile
        295                 300                 305
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gtc cag aga gtt tgc ctc cca gac tca tct ata aag ttg cca cct aaa      1016
Val Gln Arg Val Cys Leu Pro Asp Ser Ser Ile Lys Leu Pro Pro Lys
    310                 315                 320

aca agt gtg ttc gtc aca gga ttt gga tcc att gta gat gat gga cct      1064
Thr Ser Val Phe Val Thr Gly Phe Gly Ser Ile Val Asp Asp Gly Pro
325                 330                 335                 340

ata caa aat aca ctt cgg caa gcc aga gtg gaa acc ata agc act gat      1112
Ile Gln Asn Thr Leu Arg Gln Ala Arg Val Glu Thr Ile Ser Thr Asp
                345                 350                 355

gtg tgt aac aga aag gat gtg tat gat ggc ctg ata act cca gga atg      1160
Val Cys Asn Arg Lys Asp Val Tyr Asp Gly Leu Ile Thr Pro Gly Met
            360                 365                 370

tta tgt gct gga ttc atg gaa gga aaa ata gat gca tgt aag gga gat      1208
Leu Cys Ala Gly Phe Met Glu Gly Lys Ile Asp Ala Cys Lys Gly Asp
        375                 380                 385

tct ggt gga cct ctg gtt tat gat aat cat gac atc tgg tac att gta      1256
Ser Gly Gly Pro Leu Val Tyr Asp Asn His Asp Ile Trp Tyr Ile Val
    390                 395                 400

ggt ata gta agt tgg gga caa tca tgt gca ctt ccc aaa aaa cct gga      1304
Gly Ile Val Ser Trp Gly Gln Ser Cys Ala Leu Pro Lys Lys Pro Gly
405                 410                 415                 420

gtc tac acc aga gta act aag tat cga gat tgg att gcc tca aag act      1352
Val Tyr Thr Arg Val Thr Lys Tyr Arg Asp Trp Ile Ala Ser Lys Thr
                425                 430                 435

ggt atg tag tgtggattgt ccatgagtta tacacatggc acacagagct              1401
Gly Met  *


gatactcctg cgtattttgt attgtttaaa ttcatttact ttggattagt gcttttgcta   1461
gatgtcaaga agcccttcag acccagacaa atctaatatc ctgaggtggc ctttacatac   1521
gtaggaccaa accctctcta ccatgaggga agaagacaca gcaaatgaca gacagcacct   1581
attccttact cacaagggaa actgcttgtg atacttccta ataagataaa taagtggttt   1641
ccctcaattg aagacaggaa catcattttc cacaggatat gaagagctgc cagtaatgcc   1701
aaaatcttac ctcatataat acctggagca tgtgagattc ttctagtgaa aaagaacagt   1761
cttccctgaa gactcagggc ttcaacattc tagaactgat aagtggacct tcagtgtgca   1821
agaatggaga agcatgggat ttgcattatg actttgaactg ggcttatatc taataataca  1881
gagcactatc actaacctca acagttgaca ttttaaaagt ttttaaatgt atctgaactt   1941
gctgttaaca cagtgttata actcaagcac tagcttcagg aagcatgttg tgttgttaag   2001
aagcttttct gatttattct ttaacagcat cttgccatct atatgttagt agcagttggc   2061
ccagaaagga caaaaaaaaa aaaaaaaaaa aaaaaaaaa                          2100

<210> 16
<211> 438
<212> PRT
<213> Homo sapien

<400> 16
Met Met Tyr Thr Pro Val Glu Phe Ser Glu Ala Glu Phe Ser Arg Ala
 1               5                  10                  15
Glu Tyr Gln Arg Lys Gln Gln Phe Trp Asp Ser Val Arg Leu Ala Leu
            20                  25                  30
Phe Thr Leu Ala Ile Val Ala Ile Ile Gly Ile Ala Ile Gly Ile Val
        35                  40                  45
Thr His Phe Val Val Glu Asp Asp Lys Ser Phe Tyr Tyr Leu Ala Ser
    50                  55                  60
Phe Lys Val Thr Asn Ile Lys Tyr Lys Glu Asn Tyr Gly Ile Arg Ser
65                  70                  75                  80
Ser Arg Glu Phe Ile Glu Arg Ser His Gln Ile Glu Arg Met Met Ser
```

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                85                  90                  95
Arg Ile Phe Arg His Ser Ser Val Gly Gly Arg Phe Ile Lys Ser His
            100                 105                 110
Val Ile Lys Leu Ser Pro Asp Glu Gln Gly Val Asp Ile Leu Ile Val
        115                 120                 125
Leu Ile Phe Arg Tyr Pro Ser Thr Asp Ser Ala Glu Gln Ile Lys Lys
    130                 135                 140
Lys Ile Glu Lys Ala Leu Tyr Gln Ser Leu Lys Thr Lys Gln Leu Ser
145                 150                 155                 160
Leu Thr Ile Asn Lys Pro Ser Phe Arg Leu Thr Pro Ile Asp Ser Lys
                165                 170                 175
Lys Met Arg Asn Leu Leu Asn Ser Arg Cys Gly Ile Arg Met Thr Ser
            180                 185                 190
Ser Asn Met Pro Leu Pro Ala Ser Ser Ser Thr Gln Arg Ile Val Gln
        195                 200                 205
Gly Arg Glu Thr Ala Met Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu
    210                 215                 220
Gln Leu Ile Gly Ser Gly His Gln Cys Gly Ala Ser Leu Ile Ser Asn
225                 230                 235                 240
Thr Trp Leu Leu Thr Ala Ala His Cys Phe Trp Lys Asn Lys Asp Pro
                245                 250                 255
Thr Gln Trp Ile Ala Thr Phe Gly Ala Thr Ile Thr Pro Pro Ala Val
            260                 265                 270
Lys Arg Asn Val Arg Lys Ile Ile Leu His Glu Asn Tyr His Arg Glu
        275                 280                 285
Thr Asn Glu Asn Asp Ile Ala Leu Val Gln Leu Ser Thr Gly Val Glu
    290                 295                 300
Phe Ser Asn Ile Val Gln Arg Val Cys Leu Pro Asp Ser Ser Ile Lys
305                 310                 315                 320
Leu Pro Pro Lys Thr Ser Val Phe Val Thr Gly Phe Gly Ser Ile Val
                325                 330                 335
Asp Asp Gly Pro Ile Gln Asn Thr Leu Arg Gln Ala Arg Val Glu Thr
            340                 345                 350
Ile Ser Thr Asp Val Cys Asn Arg Lys Asp Val Tyr Asp Gly Leu Ile
        355                 360                 365
Thr Pro Gly Met Leu Cys Ala Gly Phe Met Glu Gly Lys Ile Asp Ala
    370                 375                 380
Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Tyr Asp Asn His Asp Ile
385                 390                 395                 400
Trp Tyr Ile Val Gly Ile Val Ser Trp Gly Gln Ser Cys Ala Leu Pro
                405                 410                 415
Lys Lys Pro Gly Val Tyr Thr Arg Val Thr Lys Tyr Arg Asp Trp Ile
            420                 425                 430
Ala Ser Lys Thr Gly Met
        435
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<210> 17
<211> 702
<212> DNA
<213> Homo sapien

<220>
<221> CDS
<222> (1)...(702)
<223> Nucleotide sequence encoding Protease Domain

<400> 17

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att gtc caa gga agg gaa aca gct atg gaa ggg gaa tgg cca tgg cag        48
Ile Val Gln Gly Arg Glu Thr Ala Met Glu Gly Glu Trp Pro Trp Gln
 1               5                  10                  15

gcc agc ctc cag ctc ata ggg tca ggc cat cag tgt gga gcc agc ctc        96
Ala Ser Leu Gln Leu Ile Gly Ser Gly His Gln Cys Gly Ala Ser Leu
            20                  25                  30

atc agt aac aca tgg ctg ctc aca gca gct cac tgc ttt tgg aaa aat       144
Ile Ser Asn Thr Trp Leu Leu Thr Ala Ala His Cys Phe Trp Lys Asn
```

```
          35                  40                  45

aaa gac cca act caa tgg att gct act ttt ggt gca act ata aca cca      192
Lys Asp Pro Thr Gln Trp Ile Ala Thr Phe Gly Ala Thr Ile Thr Pro
     50                  55                  60

ccc gca gtg aaa cga aat gtg agg aaa att att ctt cat gag aat tac      240
Pro Ala Val Lys Arg Asn Val Arg Lys Ile Ile Leu His Glu Asn Tyr
 65                  70                  75                  80

cat aga gaa aca aat gaa aat gac att gct ttg gtt cag ctc tct act      288
His Arg Glu Thr Asn Glu Asn Asp Ile Ala Leu Val Gln Leu Ser Thr
                85                  90                  95

gga gtt gag ttt tca aat ata gtc cag aga gtt tgc ctc cca gac tca      336
Gly Val Glu Phe Ser Asn Ile Val Gln Arg Val Cys Leu Pro Asp Ser
            100                 105                 110

tct ata aag ttg cca cct aaa aca agt gtg ttc gtc aca gga ttt gga      384
Ser Ile Lys Leu Pro Pro Lys Thr Ser Val Phe Val Thr Gly Phe Gly
        115                 120                 125

tcc att gta gat gat gga cct ata caa aat aca ctt cgg caa gcc aga      432
Ser Ile Val Asp Asp Gly Pro Ile Gln Asn Thr Leu Arg Gln Ala Arg
    130                 135                 140

gtg gaa acc ata agc act gat gtg tgt aac aga aag gat gtg tat gat      480
Val Glu Thr Ile Ser Thr Asp Val Cys Asn Arg Lys Asp Val Tyr Asp
145                 150                 155                 160

ggc ctg ata act cca gga atg tta tgt gct gga ttc atg gaa gga aaa      528
Gly Leu Ile Thr Pro Gly Met Leu Cys Ala Gly Phe Met Glu Gly Lys
                165                 170                 175

ata gat gca tgt aag gga gat tct ggt gga cct ctg gtt tat gat aat      576
Ile Asp Ala Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Tyr Asp Asn
            180                 185                 190

cat gac atc tgg tac att gta ggt ata gta agt tgg gga caa tca tgt      624
His Asp Ile Trp Tyr Ile Val Gly Ile Val Ser Trp Gly Gln Ser Cys
        195                 200                 205

gca ctt ccc aaa aaa cct gga gtc tac acc aga gta act aag tat cga      672
Ala Leu Pro Lys Lys Pro Gly Val Tyr Thr Arg Val Thr Lys Tyr Arg
    210                 215                 220

gat tgg att gcc tca aag act ggt atg tag                             702
Asp Trp Ile Ala Ser Lys Thr Gly Met  *
225                 230
```

<210> 18
<211> 233
<212> PRT
<213> Homo sapien

<400> 18

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Ile Val Gln Gly Arg Glu Thr Ala Met Glu Gly Glu Trp Pro Trp Gln
 1               5                  10                  15
Ala Ser Leu Gln Leu Ile Gly Ser Gly His Gln Cys Gly Ala Ser Leu
            20                  25                  30
Ile Ser Asn Thr Trp Leu Leu Thr Ala Ala His Cys Phe Trp Lys Asn
        35                  40                  45
Lys Asp Pro Thr Gln Trp Ile Ala Thr Phe Gly Ala Thr Ile Thr Pro
    50                  55                  60
Pro Ala Val Lys Arg Asn Val Arg Lys Ile Ile Leu His Glu Asn Tyr
65                  70                  75                  80
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His Arg Glu Thr Asn Glu Asn Asp Ile Ala Leu Val Gln Leu Ser Thr
85 90 95
Gly Val Glu Phe Ser Asn Ile Val Gln Arg Val Cys Leu Pro Asp Ser
100 105 110
Ser Ile Lys Leu Pro Pro Lys Thr Ser Val Phe Val Thr Gly Phe Gly
115 120 125
Ser Ile Val Asp Asp Gly Pro Ile Gln Asn Thr Leu Arg Gln Ala Arg
130 135 140
Val Glu Thr Ile Ser Thr Asp Val Cys Asn Arg Lys Asp Val Tyr Asp
145 150 155 160
Gly Leu Ile Thr Pro Gly Met Leu Cys Ala Gly Phe Met Glu Gly Lys
165 170 175
Ile Asp Ala Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Tyr Asp Asn
180 185 190
His Asp Ile Trp Tyr Ile Val Gly Ile Val Ser Trp Gly Gln Ser Cys
195 200 205
Ala Leu Pro Lys Lys Pro Gly Val Tyr Thr Arg Val Thr Lys Tyr Arg
210 215 220
Asp Trp Ile Ala Ser Lys Thr Gly Met
225 230

<210> 19
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 19
tctctcgaga aaagaattgt ccaaggaagg gaaacagcta tg 42

<210> 20
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 20
agatgagtct gggaggctaa ctctctggac tat 33

<210> 21
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 21
attcgcggcc gcctacatac cagtctttga ggcaat 36

<210> 22
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 22
atagtccaga gagttagcct cccagactca tct 33